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(54) Title: TFIIB TRANSCRIPTION FACTOR FROM CANDIDA ALBICANS

(57) Abstract

The invention encompasses a novel transcription factor from *Candida albicans*, TFIIB, a nucleic acid sequence encoding TFIIB, and methods of screening for inhibitors of *Candida albicans* growth by targeting TFIIB.

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TFIIB TRANSCRIPTION FACTOR FROM CANDIDA ALBICANS

ABSTRACT OF THE DISCLOSURE

15   The invention encompasses a novel transcription factor from *Candida albicans*, TFIIB, a nucleic acid sequence encoding TFIIB, and methods of screening for inhibitors of *Candida albicans* growth by targeting TFIIB.

The invention relates in general to transcription factors and to methods
20 for screening for antifungal agents.

BACKGROUND OF THE INVENTION

25   The yeast *Candida albicans* (*C. albicans*) is one of the most pervasive fungal pathogens in humans. It has the capacity to opportunistically infect a diverse spectrum of compromised hosts, and to invade many diverse tissues in the human body. It can in many instances evade antibiotic treatment and the immune system. Although *Candida albicans* is a member of the normal flora of the mucous membranes
30 in the respiratory, gastrointestinal, and female genital tracts, in such locations, it may gain dominance and be associated with pathologic conditions. Sometimes it produces progressive systemic disease in debilitated or immunosuppressed patients, particularly if cell-mediated immunity is impaired. Sepsis may occur in patients with compromised cellular immunity, e.g., those undergoing cancer chemotherapy or those with

lymphoma, AIDS, or other conditions. *Candida* may produce bloodstream invasion, thrombophlebitis, endocarditis, or infection of the eyes and virtually any organ or tissue when introduced intravenously, e.g., via tubing, needles, narcotics abuse, etc.

Candida albicans has been shown to be diploid with balanced lethals,

5   and therefore probably does not go through a sexual phase or meiotic cycle. This yeast appears to be able to spontaneously and reversibly switch at high frequency between at least seven general phenotypes. Switching has been shown to occur not only in standard laboratory strains, but also in strains isolated from the mouths of healthy individuals.

10   Nystatin, ketoconazole, and amphotericin B are drugs which have been used to treat oral and systemic *Candida* infections. However, orally administered nystatin is limited to treatment within the gut and is not applicable to systemic treatment. Some systemic infections are susceptible to treatment with ketoconazole or amphotericin B, but these drugs may not be effective in such treatment unless

15   combined with additional drugs. Amphotericin B has a relatively narrow therapeutic index and numerous undesireable side effects and toxicities occur even at therapeutic concentrations. While ketoconazole and other azole antifungals exhibit significantly lower toxicity, their mechanism of action, inactivation of cytochrome P_{450} prosthetic group in certain enzymes , some of which are found in humans, precludes use in

20   patients that are simultaneously receiving other drugs that are metabolized by the body's cytochrome P_{450} enzymes. In addition, resistance to these compounds is emerging and may pose a serious problem in the future.

There is a need in the art for an effective treatment of opportunistic infections caused by *Candida albicans*. Therefore, one object of the invention is to

25   provide screening assays for identifying potential inhibitors of *Candida albicans* growth. Another object of the invention is to provide screening assays and to identify potential inhibitors of *Candida albicans* growth that are based on inhibition of transcription in this organism.

Synthesis of mRNA in eukaryotes requires RNA polymerase II and

30   accessory transcription factors, some of which are general and act at most, if not all, promoters, and others of which confer specificity and control. Five general factors, a, b, d, e, and g, have been purified to homogeneity from the yeast *S. cerevisiae*, and have been identified as counterparts of human or rat factors, TFIIE, TFIIH, TFIID,

TFIIB and TFIIF, respectively. These factors assemble at a promoter in a complex with RNA polymerase II to initiate transcription. Binding studies have shown that the order of assembly of the initiation complex on promoter DNA begins with factor d (TFIID), is followed by factor e (TFIIB), and then by polymerase and the remaining

5   factors. Factors b (TFIIH), e (TFIIB) and g (TFIIF), however, bind directly to polymerase II, and as many as four of the five factors may assemble with the polymerase in a holoenzyme before promoter binding. The functional significance of interactions revealed by binding studies is not clear in that only a few percent of initiation complexes may give rise to transcripts.

10   Many aspects of transcription by RNA polymerase II are conserved between yeast and higher eukaryotes. For example, there is extensive amino acid sequence similarity among the largest subunits of the yeast, Drosophila and mammalian polymerase. Other components of the transcription apparatus, such as TATA-binding and enhancer binding factors, are in some instances interchangeable between yeast and

15   mammalian *in vitro* binding or transcription systems. There are, nonetheless, significant differences between the two systems. TATA elements are located from 40 to 120 or more base pairs upstream of the initiation site of an *S. cerevisiase* promoter, and where these elements occur, they are required for gene expression. The fact that *C. albicans* genes function in *S. cerevisiase* suggests that it also uses the 40 to 120

20   base pair spacing between the TATA element and initiation site. In contrast, mammalian (as well as *S. pombe*) TATA elements and transcription start sites are only 25 to 30 bp apart, and deletion of a TATA element does not always reduce the frequency of transcription initiation, although it may alter the initiation site. There are also varying degrees of homology between transcription factor sequences from

25   yeast and mammalian sources. Human and *S. cerevisiae* TFIIB's have 50-60% amino acid sequence identity, and also are not species interchangeable in supporting cell growth. Some of the multisubunit factors, such as RNA polymerase II, TFIIF and TFIID, contain different numbers of subunits in humans and yeast. The molecular weights of corresponding polypeptides differ in humans and yeast with sequences being

30   present in a given yeast factor that are not present in its human counterpart, and vice versa.

         Operative substitution of the same transcription factor in transcription systems of different yeast strains is not predictable. This is true despite a high degree

of amino acid sequence identity among some transcription factors from different yeast strains. For example, the ability of a given transcription factor to support efficient and accurate transcription in a heterologous yeast strain is not predictable. Li et al. (1994, Science 263:805) tested the interchangeability of *S. cerevisiae* and *S. pombe*

5   transcription factors in vitro, and report that many *S. cerevisiae* components cannot substitute individually for *S. pombe transcription factors a, e, or* RNA polymerase II, but combinations of these components were effective. In one instance, active transcription could not be reconstituted when *S. cerevisiae*-derived TFIIB was the sole substitution into a TFIIB-depleted set of factors from *S. pombe*. A TFIIB-RNA

10 polymerase II combination from *S. cerevisiae* was able to substitute, indicating that the functional interaction of these two components is not only important, but also that the activity may be dependent on species-specific determinants that cannot be complemented by either component derived from a different organism. The unpredictability in making substitutions of a given factor among different yeast strains

15 is also evident in that such substitutions are not reciprocal; that is, substitutions of *S. pombe* fractions into an *S. cerevisiae* transcription system are less effective than the reverse substitutions (Li et al., supra).

The yeast *Candida albicans* differs from most yeast strains in that it does not use the same genetic code that most organisms, whether mammalian or yeast,

20 utilize. Santos et al. (1995, Nucleic Acids Research, 23:1481) report that the codon CUG, which in the universal code is read as a leucine, is decoded as a serine in *Candida*. Therefore, any CUG codon that is decoded in *Candida albicans* as a serine, would be decoded as a leucine in the transformed *S. cerevisiae*. Any gene containing a CUG codon would therefore be translated as different amino acid sequences in

25 *Candida albicans* and *S. cerevisiae*. Such mistranslation may produce an inactive protein, since the amino acids serine and leucine have markedly different chemical properties and serine is known to be an essential residue in the active site of some enzymes. Replacement of leucine by serine at CUG encoded residues is a serious problem in the use of many reporter systems (e.g., β-galactosidase, Chloramphenicol

30 acetyltransferase, Flux) in *Candida albicans*. Previous experiments have shown that translation by *Candida* of CUG as serine instead of leucine often resulted in the production of inactive reporter proteins.

Another object of the invention is to provide an assay for screening for selective inhibition of *Candida albicans* growth and/or viability.

Yet another object of the invention is to provide a molecular target for inhibition of *Candida albicans* transcription or transcription initiation.

SUMMARY OF THE INVENTION

The invention encompasses a recombinant nucleic acid comprising a nucleic acid sequence encoding *Candida albicans* TFIIB.

The invention also encompasses a vector comprising a nucleic acid sequence encoding *Candida albicans* TFIIB, and a transformed host cell containing a nucleic acid sequence encoding *Candida albicans* TFIIB.

The invention also encompasses a recombinant polypeptide comprising *Candida albicans* TFIIB, and a fragment of *Candida albicans* TFIIB, the fragment being characterized in that it inhibits the biological activity of *Candida albicans* TFIIB in transcription initiation, or prevents the growth of *Candida albicans*.

The invention also encompasses a method for producing recombinant *Candida albicans* TFIIB, comprising culturing a host cell transformed with a nucleic acid encoding *Candida albicans* TFIIB under conditions sufficient to permit expression of the nucleic acid encoding *Candida albicans* TFIIB, and isolating *Candida albicans* TFIIB.

The invention also encompasses a screening method for identifying an inhibitor of *Candida albicans* growth, comprising detecting inhibition of mRNA transcription in an *in vitro* transcription assay comprising a DNA template, RNA polymerase II, recombinant *Candida albicans* TFIIB, and a candidate inhibitor, wherein production of an mRNA transcript complementary to the DNA template occurs in the absence of the candidate inhibitor. Preferably, the assay will also include *C. albicans* TBP.

The invention also encompasses a screening method for identifying an inhibitor of *Candida albicans* growth, comprising detecting in the presence of a candidate inhibitor inhibition of formation of a complex comprising a DNA template recombinant *Candida albicans* TFIIB and TBP, wherein in the absence of the candidate inhibitor, formation of the complex occurs.

The invention also encompasses a screening method for identifying an inhibitor of *Candida albicans* growth, comprising detecting in the presence of a candidate inhibitor inhibition of formation of a complex comprising *Candida albicans* TFIIB and *Candida albicans* TBP, wherein in the absence of the candidate inhibitor formation of the complex occurs. Preferably, the complex will include a DNA template.

The invention also encompasses a screening method for identifying an inhibitor of *Candida albicans* growth, comprising detecting in the presence of a candidate inhibitor inhibition of formation of a complex comprising RNA polymerase II, *Candida albicans* TBP, and *Candida albicans* TFIIB, wherein in the absence of the candidate inhibitor formation of the complex occurs. Preferably, the complex may also include a DNA template; and RNA polymerase II from *C. albicans*.

In the above-described screening methods, detection may be performed in the presence of a plurality of candidate inhibitors. In screening methods of the invention which involve screening of a plurality of candidate inhibitors, the plurality of inhibitors may be screened together in a single assay or individually using multiple simultaneous individual detecting steps.

The invention also encompasses a method of preventing *Candida albicans* growth in culture, comprising contacting the culture with an inhibitor that selectively inhibits the biological activity of *Candida albicans* TFIIB.

The invention also encompasses a method of preventing *Candida albicans* growth in a mammal, comprising contacting the mammal with an inhibitor that selectively inhibits the biological activity of *Candida albicans* TFIIB.

As used herein, "inhibition" refers to a reduction in the parameter being measured, whether it be *Candida albicans* growth or viability, *Candida albicans* TFIIB-mediated transcription, or formation of a *Candida albicans* TFIIB transcription complex. The amount of such reduction is measured relative to a standard (control). Because of the multiple interactions of *Candida albicans* TFIIB in transcription initiation, the target product for detection varies with respect to the particular screening assay employed. Three preferred detection products presented in this disclosure are; a) newly transcribed mRNA, b) a DNA-TFIIB complex, and c) a TBP-TFIIB-RNA polymerase complex. "Reduction" is defined herein as a decrease of at least 25% relative to a control, preferably of at least 50%, and most preferably of at least 75%.

As used herein, "growth" refers to the normal growth pattern of _Candida albicans_ , i.e., to a cell doubling time of 60-90 minutes. "Viability" refers to the ability of _Candida albicans_ to survive in culture for 48 hours.

"Biological activity" refers to the ability of TFIIB to form a transcription complex with a DNA template or other proteins of the transcription complex, or to interact with other transcription components so as to permit initiation of transcription.

"DNA template" refers to double stranded DNA and, where indicated by the particular binding assay to single stranded DNA, at least 10 nucleotides in length, that may be negatively supercoiled, possesses a promoter region, and contains a yeast TATA consensus region upstream of the promoter . DNA templates useful herein preferably contain a TATA sequence that is located from 40 to 120 or more base pairs upstream of the initiation site (distance measured from the first T of the TATA element to the 5'-most initiation site). An especially efficient DNA template for use in methods of the invention involving transcription is devoid of guanosine residues, and therefore a "G-minus" or "G-less" cassette is preferred (Sawdago and Roeder, 1985, PNAS 82:4394-4398).

"mRNA transcript" refers to a full-length transcript as well as to truncated transcripts, oligonucleotide transcripts and dinucleotide RNAs.

"Formation of a complex" refers to the binding of TFIIB to other transcription factors (i.e., protein-protein binding) as well as to binding of TFIIB to a DNA template; such binding will, of course, be a non-covalent association.

Other features and advantages of the invention will be apparent from the description, preferred embodiments thereof, the drawings, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 presents the nucleotide and amino acid sequences of the _Candida albicans_ transcription factor TBP.

Fig. 2 presents nucleotide and amino acid sequence of the _Candida albicans_ transcription factor TFIIB.

DESCRIPTION

The invention is based on the discovery of a novel protein, _Candida albicans_ TFIIB, and on the isolation of recombinant DNA encoding _Candida albicans_ transcription factor TFIIB. Because TFIIB is essential for viability of the cell, a

compound that blocks the biological activity of the protein is expected to have fungicidal properties. Therefore, the invention is also based on the development of assays for screening from inhibitors of TFIIB.

5   Isolation and Characterization of the *Candida albicans* TBP and TFIIB Genes

Given the unpredictability with respect to operative substitutions of a given transcription factor among different yeast strains, one cannot assume that strategies for cloning of the gene encoding a given transcription factor which are based on factor function, such as genetic complementation, will work. Other cloning strategies, which

10   do not require functional complementation, such as those based on homology at the nucleic acid level, may be utilized in an attempt to circumvent a requirement for factor function. For example, Southern hybridization of specific sequences to a library carried in *E. coli* and PCR amplification of potentially highly homologous regions of a gene are two strategies that have been successfully used to clone homologous genes from different

15   organisms. To ascertain the likelihood of success of these or similar methods, we performed a Southern hybridization experiment where a radiolabeled probe containing the entire *S. cerevisiae* coding sequence of TBP (*SPT15*) was hybridized to genomic DNA preparations from *S. cerevisiae* and *Candida albicans* that were digested with various restriction enzymes. At low stringency (0.2X SSC, room temperature hybridization) the

20   probe efficiently hybridized as expected to known restriction bands in the *S. cerevisiae* digests, but did not detectably hybridize to any restriction band of the *Candida albicans* digests. The *Saccharomyces* sequences were detectable on an autoradiograph with less than 10 minutes of exposure. By contrast, even with one week of exposure, there was no detectable hybridization of the same probe to the *Candida albicans* DNA. The conclusion

25   from these observations is that it is likely that the DNA sequence of the *Candida albicans* gene had diverged quite significantly from the *S. cerevisiae* sequence, and thus Southern hybridization, PCR strategies or other cloning methods based on hybridization of complementary nucleic acid sequences are unlikely to lead to cloning of the *Candida albicans* homolog of SPT15.

30   The approach used to clone the *Candida albicans* homolog of TFIIB involved genetic complementation of mutant *S. cerevisiae* strains. A library of *Candida albicans* genomic sequences was introduced into a strain of *S. cerevisiae* that contained

a mutated TFIIB gene (SUA7). This mutant strain was capable of growth at 30⁰ C, but was non-viable at 37⁰ C, due to a temperature sensitive mutation in the TFIIB gene. Following transformation of the library into the strain, the cells were grown at 37⁰ C, and the colonies which grew at this non-permissive temperature were further studied as

5 potentially carrying a *Candida albicans* homolog of the defective gene. Plasmids were purified from the various isolates which were viable at 37°C. After candidate clones were isolated by growth at the nonpermissive temperature, the library plasmid was recovered from the cell and retested to confirm that the *C. albicans* sequences on the plasmid were substituting for the *S. cerevisiae* gene. Subclones of *C. albicans* sequences were

10 constructed by standard cloning methods, and the minimal *Candida* DNA sequence that substituted was sequenced using standard methods. Digestion of these plasmids revealed a common DNA fragment approximately 1.35 kb in length, which when subcloned into pRS316 proved to complement multiple independent SUA7 strains of *S. cerevisiae*. This DNA fragment was sequenced, and confirmed *C. albicans* SUA7 sequence homology to

15 *S. cerevisiae* SUA7.

The nucleotide sequence encoding *Candida albicans* TBP and the predicted amino acid sequence of the encoded protein are presented in Fig. 1 (SEQ ID NOS: 1 and 2). The nucleotide sequence encoding *Candida albicans* TFIIB and the predicted amino acid sequence of the encoded protein are presented in Fig. 2 (SEQ ID NOS: 3 and 4).

20

Methods For Screening Potential Inhibitors of *Candida albicans* Growth and/or Viability

Because TFIIB is essential for transcription initiation, the recombinant *Candida albicans* TFIIB gene and recombinant protein encoded by this gene may be utilized in screening assays for inhibitors of *Candida albicans* growth and viability. The

25 screening assays of this invention detect inhibition of the *Candida albicans* TFIIB-mediated transcription initiation, either by measuring inhibition of transcription, transcription initiation, or initiation complex formation, or by assaying formation of a protein/DNA or a protein/protein complex.

30

EXAMPLE 1

Screening for Inhibitors of Transcription

a) Transcription Assay Components.

An *in vitro* transcription assay consisting of the minimal components

5   necessary to synthesize an mRNA transcript from a DNA template can be used to screen
for inhibition of mRNA production. The elements of such an assay consist of; a) a DNA
template, b) RNA polymerase II, c) recombinant *Candida albicans* TFIIB, and d) a TBP
which is preferably *Candida albicans* TBP.   In order to increase the efficiency of
transcription, additional components of the transcription complex may be included, as

10   desired; e.g., TFIIE, TFIIF, TFIIH, etc.

Parvin and Sharp (*Cell* 73, 533-540, 1993) have reconstituted gene
transcription *in vitro* with a minimal reaction containing a DNA template, RNA
polymerase II, TFIIB, and TBP. For efficient transcription under minimal conditions, the
DNA template (a) is supercoiled, and (b) possesses a promoter region containing a TATA

15   consensus region. Additionally, Lue et al. (*Science* 246, 661-664, 1989) have determined
that transcription may be detected most efficiently with a DNA template devoid of
guanosine residues (a G-minus or G-less cassette). Promoter dependence is demonstrated
by the loss of signal when a plasmid lacking promoter sequences is utilized as a template.
Correct initiation is demonstrated by the production of a band with a mobility consistent

20   with the size of the expected product on denaturing polyacrylamide electrophoresis gels.

As stated above, *Candida albicans* TFIIB forms a transcription initiation
complex with RNA polymerase II.   Therefore, it is desired that an *in vitro* transcription
assay according to the invention contain RNA polymerase II. Although it is possible to
perform an inhibitor screening assay using RNA polymerase II from a yeast strain other

25   than *Candida albicans*, e.g., *S. cerevisiae*, it is most desirable to use a homologous assay
in which the transcription complex components are from *Candida albicans* .

A method for S. cerevisiae RNA polII purification is described in Edwards
et al. (*Proc. Natl. Acad. Sci. USA 87*: 2122-2126 (1990)). Alternatively, highly purified
RNA polymerase II from *Candida albicans* was provided as follows.

30   RNA polymerase II activity was measured in reactions containing 50 mM
Tris-Cl, pH 7.9 (4° C), 50 mM $(NH_4)_2$ SO_4, 2.5 mM $MnCl_2$, 0.1 mM EDTA, 5 mM
DTT, 100 μg/ml BSA, 0.6 mM ATP, CTP and GTP, 25 μM UTP (2.5 μCi) [α-^{32}P] UTP
and 100 μg/ml heat-denatured calf thymus DNA in a final volume of 50 μl. Reactions

were incubated for 60 min. at 30⁰ C and terminated by addition of 50 μl 15% (w/v) trichloroacetic acid. Acid-insoluble radioactivity was collected by filtration through glass fiber filters and quantified by liquid scintillation spectrophotometry. One unit of RNA polymerase activity catalyzes the incorporation of 1 pmol of UTP into acid-insoluble

5   material in 60 min. under the conditions described above.

Candida albicans was obtained from the American Type Culture Collection (ATCC 10231) and cultured in YPD medium (Current Protocols in Molecular Biology, Vol. 2, 13, Suppl. 19 (1989)) at 30⁰ C with vigorous agitation and aeration. All procedures were carried out at 4⁰ C using 18 liter cultures. Cells were harvested by

10   centrifugation (5000 rpm, 10 min., Sorvall H6000 rotor), washed once with ~ 1l ice-cold deionized water and repelleted as above. The cell pellet (200-300 g wet weight) was thoroughly resuspended in a volume of Buffer A (50 mM Tris-HCl, pH 7.9, 4⁰ C, 10% glycerol, 1 mM EDTA, 5 mM $MgCl_2$, and protease inhibitor) containing 300 mM $(NH_4)_2$ SO_4 equivalent to the packed volume of cells (determined by weight assuming a density

15   of 1 g/ml cells). Resuspended cells were either processed immediately as described below or frozen by pipetting into liquid N_2 and stored at -80 C. Frozen cells were thawed on ice prior to proceeding. Following the addition of NP-40 to a final concentration of 0.1%, cells were disrupted by grinding with 1 ml acid-washed glass beads/ml cell suspension (Sigma, 400-625 μM) using 12 bursts of 30 sec. each in a Bead Beater

20   (BioSpec). Glass beads were allowed to settle out and the supernatant was centrifuged at 30,000 x g for 40 min. Solid $(NH_4)_2$ SO_4 was slowly added to a final concentration of 0.4 g/ml supernatant and the resulting precipitate was pelleted by centrifugation at 100,000 x g for 30 min. The pellet was resuspended with a volume of Buffer A sufficient to yield a conductivity equivalent to Buffer A containing 75 mM $(NH_4)_2$ SO_4.

25   Following centrifugation of the resuspension at 10,000 x g for 10 min, this supernatant ~ 1-1.5 mg protein/ml) was loaded onto a 300 ml DE-52 DEAE-cellulose column equilibrated with Buffer A containing 75 mM $(NH_4)_2$ SO_4. After washing with 5 column volumes Buffer A containing 75 mM $(NH_4)_2$ SO_4, and 5 column volumes Buffer A containing 0.15 M $(NH_4)_2$ SO_4, RNA polymerase II was eluted with 5 column volumes

30   Buffer A containing 0.4 M $(NH_4)_2$ SO_4. Fractions were collected containing the peak of protein, determined by absorbance at 280 nm and pooled. The pool was dialyzed against Buffer A containing 20% glycerol for 3 hr. at 4⁰ C.

The 0.4 M $(NH_4)_2$ SO_4 eluate from DEAE-cellulose (261 mg protein, 290 ml) was diluted with sufficient Buffer A to lower the conductivity to the equivalent of Buffer A containing 0.15 M $(NH_4)_2$ SO_4, centrifuged at 10,000 x g for 10 min. and the supernatant was loaded at a flow rate of 30 ml/hr onto an 30 ml DEAE-cellulose column

5 equilibrated with Buffer A containing 0.15 M $(NH_4)_2$ SO_4. After washing with 3 column volumes of Buffer A containing 0.15 M $(NH_4)_2$ SO_4, the column was developed with a 200 ml linear gradient of 0.15 - 0.4 M$(NH_4)_2$ SO_4 in Buffer A at a flow rate of 45 ml/hr. Fractions from the single peak of amanitin-sensitive RNA polymerase activity, eluting around 0.22 M $(NH_4)_2$ SO_4, were pooled (21.1 mg protein, 45 ml) and loaded directly

10 onto a 5 ml Heparin agarose column equilibrated with Buffer A containing 0.2 M $(NH_4)_2$ SO_4. The column was washed with 3 column volumes of Buffer A containing 0.2 M $(NH_4)_2$ SO_4 and developed with an 80 ml linear gradient of 0.2 - 0.6 M $(NH_4)_2$ SO_4 in Buffer A. The active fractions, which eluted at approximately 0.42 M $(NH_4)_2$ SO_4 were pooled (2.0 mg protein, 15 ml), frozen in 300 μl aliquots in liquid N_2, and stored at -80°

15 C where activity was stable for at least 6 months.

Purification of protein initiation factors used in the assay is accomplished by standard methods known in the art (e.g., phosphocellulose chromatography followed by gel filtration), as described in (*Nature* 346, 387-390 (1990)).

To screen for *Candida albicans* TFIIB-mediated transcription inhibition, a

20 transcription assay is reconstituted using recombinant *Candida albicans* TFIIB. *Candida albicans* TFIIB is expressed in and purified from *E. coli* as described in Buratowski, 1993, *Proc. Natl. Acad. Sci.* 90:5633. Supercoiled plasmid DNA containing the CYC1 promoter linked to the G-less cassette described by Lue *et al.* (*Science* 246, 661-664 (1989)), is purified by standard methods for purification of supercoiled circular DNA

25 (Current Protocols in Molecular Biology, Vol. 2, 13, Suppl. 19 (1989)). 10 - 100 ng of *Candida albicans* TFIIB, 10 - 100 ng of *Candida albicans* TBP, 10 - 100 ng *Candida albicans* RNA polymerase II and 1 μg plasmid DNA are added to 50 μl reaction mixtures containing 50 mM HEPES, pH 7.5, 10% glycerol, 90 mM potassium glutamate, 0.75% polyethylene glycol (molecular weight 3350), 10 mM magnesium acetate, 5 mM EGTA,

30 5 mM DTT, 0.4 mM ATP, 0.4 mM CTP, 10 μM [α-^{32}P]UTP, 0.2 mM 3'-O-methyl-GTP, and containing or lacking a candidate inhibitor molecule. Reactions are incubated at 30° C for 30 - 60 min. and RNA synthesis is detected as described below.

b) Detection of Transcribed RNA.

The detection of newly transcribed RNA is achieved by standard methods (Current Protocols in Molecular Biology, Vol. 1, 4.10, Suppl 24 (1989)). As one example, RNA synthesis can be detected as incorporation of a radioactively or fluorescently labeled nucleotide into higher molecular weight RNA products, determined by one of the following methods: 1) acid-insoluble labeled material quantitated by the appropriate method (e.g. scintillation counting for radioactive precursors, fluorometry for fluorescent precursors); 2) labeled reaction product that hybridizes to oligonucleotides complementary to the correctly initiated transcript (i.e., northern blot analysis); 3) the presence of a labeled band with the appropriate mobility detected by autoradiography, on denaturing polyacrylamide electrophoresis gels: 4) any other method that discriminates mononucleotides from polynucleotides, where polynucleotides are the desired RNA product. Such methods may utilize one or more well known techniques of molecular biology (Current Protocols in Molecular Biology, Vol. 2, 13, Suppl. 19 (1989)), for example; UV analysis; affinity systems (e.g., affinity chromatography, nitrocellulose filtration, biotin/streptavidin systems, immunoaffinity,) (Current Protocols in Molecular Biology, Vol. 2, 13, Suppl. 19 (1989)); and high performance liquid chromatography.

The inclusion of an inhibitor molecule that interferes with _Candida albicans_ TFIIB biological activity inhibits transcription. In this assay inhibition is measured as a reduction in the amount of mRNA transcript produced relative to the amount of mRNA transcript produced in the absence of the inhibitor (the positive control). A decrease in amount of mRNA transcript is indicative of an inhibitor. The determination of effective levels of mRNA transcript inhibition is described below.

EXAMPLE 2

Screening for Inhibition of DNA-Protein Complex Formation

A DNA-protein binding assay consisting of the minimal components necessary to permit DNA-_Candida albicans_ TFIIB association to occur can be used to screen for inhibition of the formation of the DNA-TBP-_Candida albicans_ TFIIB complex during transcription initiation. The components of such an assay include: a) a DNA template, b) recombinant _Candida albicans_ TFIIB, c) TBP, preferably from C. albicans, and optionally d) a candidate _Candida albicans_ TFIIB inhibitor.

The inclusion of an inhibitor molecule that interferes with the interaction between the _Candida albicans_ TFIIB and the DNA template inhibits transcription initiation. The inhibitor may interact directly with the _Candida albicans_ TFIIB protein, and/or it may interact with TBP and/or with the DNA template at the site of TFIIB/TBP

5   binding. In this assay inhibition is measured as a reduction in the amount of DNA-TBP-TFIIB complex produced relative to the amount of DNA-TBP-TFIIB complex produced in the absence of the inhibitor (the positive control). A decrease in the amount of DNA-TBP-TFIIB complex is indicative of an inhibitor. Determination of effective levels of DNA-TBP-TFIIB inhibition is described below.

10   One DNA binding assay is constructed as follows. 10 - 100 ng _Candida albicans_ TFIIB, expressed in and purified from _E. Coli_ as described above, is incubated with 0.5 ng labeled (e.g. radioactively or fluorescently labeled) oligonucleotide containing a TATA element such as the one described by Buratowski _et al._ (_Cell_ 56, 549-561 (1989) and 10 - 100 ng _Candida albicans_ TBP in reactions containing 10 - 20 mM HEPES (or

15   equivalent), pH 7.5 - 8.0, 5 mM $MgCl_2$, 12% glycerol, 10 mM dithiothreitol (DTT), 100 μg/ml BSA, 5 - 20 μg/ml poly (dG-dC):(dG-dC) and a candidate inhibitor of complex formation. Reactions are incubated at 30^0 C for 30-60 min.

Formation of a DNA-TBP-TFIIB complex may be detected as retention of labeled DNA (the label being detected by an appropriate methodology such as scintillation

20   counting for radiolabeled DNA or fluorometry for fluorescently labeled DNA) utilizing known affinity methods for protein immobilization (e.g., biotin/streptavidin, nitrocellulose filtration, affinity chromatography, immunoaffinity). Nonretention of labeled DNA due to the failure of _Candida albicans_ TFIIB-TBP-DNA complex formation is indicative of an effective inhibitor.

25   Complex formation may also be detected as retention of labeled _Candida albicans_ TFIIB (e.g. radioactively, fluorescently) utilizing known methods for immobilizing DNA. Nonretention of labeled _Candida albicans_ TFIIB due to the failure of _Candida albicans_ TFIIB-TBP-DNA complex formation is indicative of an effective inhibitor. The preceding two methods are suitable for high-throughput chemical compound

30   library screening applications such as those commonly used in drug discovery.

A third example of detecting DNA/protein complex formation involves detection of an electrophoretic mobility shift of labeled DNA on 4% polyacrylamide gels containing 5% (v/v) glycerol, 25 mM Tris, 100 mM glycine, 1mM EDTA, 5 mM $MgCl_2$,

pH 8.3 in the presence of _Candida albicans_ TFIIB and TBP. The position of the labeled oligonucleotide is detected by appropriate methods (e.g., autoradiography for radioactive oligonucleotide). The absence or deviation of the expected mobility shift due to DNA-_Candida albicans_ TFIIB complex formation is indicative of an effective inhibitor.

5   Finally, other methods for detecting or separating DNA-protein complexes may be used, including UV crosslinking analysis, high performance liquid chromatography, phage display technology (U.S. Patent No. 5,403,484. Viruses Expressing Chimeric Binding Proteins), and surface plasmon resonance (Biacore, Pharmacia Biosensor, North America) as described below.

10

EXAMPLE 3
Screening for Inhibition of Protein-Protein Complex Formation

          A protein-protein binding assay consisting of the minimal components necessary to permit _Candida albicans_ TBP-_Candida albicans_ TFIIB binding to occur can be used to screen for inhibition of the formation of the _Candida albicans_ TBP-_Candida albicans_ TFIIB complex during transcription initiation. The elements of such an assay consist of; a) recombinant _Candida albicans_ TFIIB, b) TBP, preferably a recombinant _Candida albicans_ TBP, and optionally c) a candidate inhibitor of binding.

          The inclusion of an inhibitor molecule that interferes with the interaction between the _Candida albicans_ TBP and _Candida albicans_ TFIIB inhibits transcription initiation. The inhibitor may interact with the _Candida albicans_ TBP or TFIIB protein and thus induce a conformational change which prevents binding, or it may directly inhibit the interaction of _Candida albicans_ TFIIB and TBP proteins. In this assay, inhibition is measured as a reduction in the amount of _Candida albicans_ TBP-TFIIB complex produced relative to the amount of _Candida albicans_ TBP-TFIIB complex produced in the absence of the inhibitor (the positive control). A decrease in the amount of TFIIB-TBP complex is indicative of an inhibitor. Determination of effective levels of inhibition of _Candida albicans_ TBP-TFIIB binding is described below.

          One assay for formation of _Candida albicans_ TBP-TFIIB complex is provided as follows. 10 - 100 ng _Candida albicans_ TFIIB and 10 - 100 ng _Candida albicans_ TBP are expressed in and purified from _E. coli_ as described above, and are added to reactions containing 10 - 20 mM HEPES (or equivalent), pH 7.5 - 8.0, 5 mM

MgCl$_2$, 12% glycerol, 10 mM dithiothreitol (DTT) 100 μg/ml BSA, and a candidate inhibitor. The mixture is then incubated at 30° C for 30 - 60 min.

Formation of a complex comprising _Candida albicans_ TBP and _Candida albicans_ TFIIB may be detected by an electrophoretic mobility shift of labeled (e.g. radioactive or fluorescent) TBP or TFIIB on 4% polyacrylamide gels containing 5% (v/v) glycerol, 25 mM Tris, 100 mM glycine, 1mM EDTA, 5 mM MgCl$_2$, pH 8.3 in the presence of the unlabeled partner. The position of the labeled partner is detected by appropriate methods (e.g., autoradiography for radioactive oligonucleotide). The absence or deviation of the expected mobility shift due to _Candida albicans_ TFIIB-TBP complex formation is indicative of an effective inhibitor.

Formation of a complex comprising _Candida albicans_ TBP and _Candida albicans_ TFIIB may be detected as retention of labeled TBP utilizing known affinity methods for immobilizing the _Candida albicans_ TFIIB protein (e.g., biotin/streptavidin, nitrocellulose filtration, affinity chromatography, immunoaffinity). The failure of formation of the _Candida albicans_ TFIIB-TBP complex is indicative of inhibition, and is indicated by nonretention of labeled TBP. Alternatively, the immobilized element may be _Candida albicans_ TBP and the labeled partner _Candida albicans_ TFIIB.

In the above example, a stronger signal may be conferred in the presence of both TBP and TFIIB and, in addition, a DNA template containing a TATA element. The complex is then quantitated by autoradiography, Phosphorimager technology, or scintillation counting for radioactively labeled factors, fluorometry for fluorescently labeled factors, luminometry for factors labeled with ligands that are detected using chemiluminescent or phosphorescent probing methodologies, or other similar detection methods or materials labeled as described above that are standard in the art.

Other methods for detecting or separating protein-protein complexes may be used, including UV crosslinking analysis, high performance liquid chromatography, phage display technology, and surface plasmon resonance as described herein.

EXAMPLE 4

Assay for Formation of TBP-TFIIB-RNA Polymerase II-DNA Complex

Formation of a TBP, TFIIB, RNA polymerase II, DNA complex is known to be markedly stimulated by the addition of another factor, TFIIF. Previous data indicates that TFIIF from _S. cerevisiae_ can function in species as distantly related as

Schizosaccharomyces pombe and humans, strongly suggesting that this factor can functionally replace its *C. albicans* homolog. Accordingly, this factor is purified from *S. cerevisiae* by published methods (Sayre, 1992, J. Biol. Chem. 267:23383) and used to reconstitute formation of a complex containing *C. albicans* TBP, TFIIB, RNA polymerase II and promoter containing DNA such as that described for reconstitution of the TFIIB-TBP-DNA complex.

Complex formation is carried out in reactions containing, for example, 10 - 100 ng *Candida albicans* TBP, 10 - 100 ng *Candida albicans* TFIIB, 10 - 100 ng *Candida albicans* RNA polymerase II, 10 - 100 ng *S. cerevisiae* TFIIF, 0.5 ng double-stranded TATA element containing-oligonucleotide (same as that used for TFIIB-TBP-DNA complex assay), 10 - 20 mM HEPES (or equivalent), pH 7.5 - 8.0, 5 mM $MgCl_2$, 12% glycerol, 10 mM dithiothreitol (DTT), 100 μg/ml BSA, 5 - 20 μg/ml poly (dG-dC); (dG-dC) and compound(s) to be tested for inhibitory activity. Following incubation at 30^0 C for 30 - 60 min, complexes are detected by one of the methods described above for the TBP-TFIIB-DNA complex. The TBP-TFIIB-RNA polymerase II-DNA complex has a slower electrophoretic mobility than the TBP-TFIIB-DNA complex identified by using the electrophoretic method. In addition, complex formation can be detected as TBP, TFIIB-dependent retention of RNA polymerase II activity (measured by incorporation of labeled nucleotide precursors into acid-insoluble product using the assay for RNA polymerase activity described in the RNA polymerase II purification protocol above) on a matrix with bound TATA-element containing DNA. The IC_{50} of inhibitory compounds will be determined by titration into reactions reconstituted as described above. The IC_{50} of these compounds against reactions reconstituted with human TBP, TFIIB and RNA polymerase II will also be determined by the same method. Human RNA polymerase II and TFIIF are purified as described previously (Flores et al., 1990, J. Biol. Chem. 265:5629-5634; Reinberg et al., J. Biol. Chem 262:3310-3321). Those compounds whose IC_{50} against reactions containing *C. albicans* factors is $\le$ 1/5 of their IC_{50} against reactions reconstituted with human factors will be tested for their ability to inhibit *C. albicans* growth as described below.

EXAMPLE 5

Phage Display Inhibitor Screening

In addition to the above mentioned standard techniques of the art, other technologies for molecular identification can be employed in the identification of inhibitor molecules. One of these technologies is phage display technology (U.S. Patent No. 5,403,484. Viruses Expressing Chimeric Binding Proteins). Phage display permits identification of a binding protein against a chosen target. Phage display is a protocol of molecular screening which utilizes recombinant bacteriophage. The technology involves transforming bacteriophage with a gene that encodes an appropriate ligand (in this case, a candidate inhibitor) capable of binding to the target molecule of interest. For the purposes of this disclosure, the target molecule may be *Candida albicans* TFIIB, or a DNA-protein or protein-protein complex formed using TBP and/or TFIIB, as described herein. The transformed bacteriophage (which preferably is tethered to a solid support) express the candidate inhibitor and display it on their phage coat. The cells or viruses bearing the candidate inhibitor which recognize the target molecule are isolated and amplified. The successful inhibitors are then characterized.

Phage display technology has advantages over standard affinity ligand screening technologies. The phage surface displays the microprotein ligand in a three dimensional conformation, more closely resembling its naturally occurring conformation. This allows for more specific and higher affinity binding for screening purposes.

EXAMPLE 6

Biospecific Interaction Analysis

A second relatively new screening technology which may be applied to the inhibitor screening assays of this invention is biospecific interaction analysis (BIAcore, Pharmacia Biosensor AB, Uppsala, Sweden). This technology is described in detail by Jonsson et al. (Biotechniques 11:5, 620-627 (1991)). Biospecific interaction analysis utilizes surface plasmon resonance (SPR) to monitor the adsorption of biomolecular complexes on a sensor chip. SPR measures the changes in refractive index of a polarized light directed at the surface of the sensor chip.

Specific ligands (i.e., candidate inhibitors) capable of binding to the target molecule of interest (i.e., *Candida albicans* TFIIB or a protein-protein or protein-DNA complex containing TFIIB) are immobilized to the sensor chip. In the presence of the

target molecule, specific binding to the immobilized ligand occurs. The nascent immobilized ligand-target molecule complex causes a change in the refractive index of the polarized light and is detected on a diode array. Biospecific interaction analysis provides the advantages of: 1) allowing for label-free studies of molecular complex formation; 2) studying molecular interactions in real time as the assay is passed over the sensor chip; 3) detecting surface concentrations down to 10 pg/mm^2; detecting interactions between two or more molecules; and 4) being fully automated (Biotechniques 11:5, 620-627 (1991)).

EXAMPLE 7

High Throughput Screening of Potential Inhibitors

It is contemplated according to the invention that the screening methods disclosed herein encompass screening of multiple samples simultaneously, also referred to herein as 'high throughput' screening. For example, in high throughput screening, from several hundred to several thousand candidate inhibitors may be screened in a single assay. An example of high throughput screening assay useful according to the invention is as follows.

A protein A (pA)- *Candida albicans* TFIIB fusion protein is generated by inserting the coding sequence of TFIIB in frame downstream of the pA coding sequence of the plasmipRIT2T (Pharmacia Biotech). The fusion construct is induced, and the resultant recombinant protein is extracted and purified according to the manufacturer's recommended conditions. This procedure can also be carried out for the preparation of a pA- *Candida albicans* TBP fusion protein except that the downstream coding sequence is that of TBP protein; all other steps would remain the same.

A Dynatech Microlite 2 microtiter plate, or equivalent high protein-binding capacity plate, is coated with 1 µg/well human IgG by incubating 300 µl 3.33 µg/ml human IgG (Sigma) in coating buffer (0.2 M sodium carbonate, pH 9.4) in the well for 4-12 hr at 4°C. The coating buffer is then decanted and the wells are washed five times with 300 µl PBS. 300 µl blocking buffer (SuperBlock™ blocking buffer; Pierce) containing 3.33 µg/ml pA- TFIIB or pA-TFIIB are added and the plate is incubated for 4 or more hours at 4°C. The plates may be stored in this form at 4°C until ready for use. When ready for use the plates are washed five times with 300 µl PBS. Test compound at a final concentration of 20-200 µM and labeled TFIIB or TBP (i.e., nonfusion protein), whichever is not added during the coating step, and 10 - 1000 fmol DNA

containing a TATA sequence, are suspended in HEG buffer containing 200 μg/ml BSA in a total volume of 150 μl and are added and the reaction is incubated at room temperature with gentle agitation for 60 min. The plate is then washed five times with PBS using a Dynatech plate washer or equivalent. Bound labeled protein is quantitated by adding 250 μl Microscint (Packard) per well and is counted in a microtiter plate-compatible scintillation spectrophotometer.

As an alternative, the protein A fusion and the second, non-fusion protein can be incubated in the presence of test compound in polypropylene microtiter plates under the same buffer and incubation conditions described above. The reaction mix is then transferred to the wells of a microtiter plate coated with human IgG (which is prepared as described above, and is stored in blocking buffer and is washed five times with 300 μl PBS immediately before use) and is incubated for 60 min at room temperature with gentle agitation. Retention of radioactive protein is quantified as above.

Interaction of TBP and TFIIB, which is measured as retention of radioactivity on the plate, is dependent on human IgG coating the plate and wild-type _Candida albicans_ TBP or TFIIB, one of which must be fused to pA. Candidate inhibitors or extracts that inhibit retention of radioactivity by more than 30% are identified and the inhibitory activity is further purified if necessary. Inhibitors identified as described above are then tested for their ability to inhibit _Candida albicans_ TFIIB-dependent transcription in an _in vitro_ transcription system such as that described herein, and also may be tested for their ability to inhibit _Candida albicans_ growth.

Other fusion or modified protein systems that are contemplated include, but are not limited to, glutathione-S-transferase, maltose binding protein, influenza virus hemaglutinin, FLAG™ and hexahistidine fusions to _Candida albicans_ TBP or _Candida albicans_ TFIIB which are prepared, expressed, and purified by published methods or biotinylated _Candida albicans_ TBP or TFIIB which are prepared using reactive biotin precursors available commercially. The purified fusion or modified protein is immobilized on a microtiter plate containing the appropriate ligand for each fusion protein (e.g. glutathione, amylose, CA157 antibody, etc., respectively) and the assay is carried out and the results evaluated in essentially the same manner as described above.

EXAMPLE 8

Candidate Inhibitors

A "candidate inhibitor," as used herein, is any compound with a potential to inhibit *Candida albicans* TFIIB-mediated transcription initiation or complex formation. A candidate inhibitor is tested in a concentration range that depends upon the molecular weight of the molecule and the type of assay. For example, for inhibition of protein/protein or protein/DNA complex formation or transcription initiation, small molecules (as defined below) may be tested in a concentration range of 1pg - 100 ug/ml, preferably at about 100 pg - 20 ug/ml; large molecules, e.g., peptides, may be tested in the range of 10 ng - 100 ug/ml, preferably 100 ng - 10 ug/ml.

Inhibitors of *Candida albicans* growth or viability may target the novel transcription factor described herein, TFIIB, or it may target a protein or nucleic acid that interacts with the novel transcription factor so as to prevent the natural biological interaction that occurs *in vivo* and leads to transcription initiation in Candida. Thus, an inhibitor identified as described herein will possess two properties: 1) at some concentration it will inhibit *Candida albicans* growth or viability; and 2) at the same concentration, it will not significantly affect the growth of mammalian, particularly human, cells.

Candidate inhibitors will include peptide and polypeptide inhibitors having an amino acid sequence based upon the novel TFIIB sequences described herein. For example, a fragment of TFIIB may act as a competitive inhibitor with respect to TFIIB binding to other proteins involved in Candida transcription, e.g., RNA polymerase II, TBP, or with respect to binding of the transcription complex to the DNA template. One such candidate fragment is a fragment of TFIIB containing a classic zinc finger motif (sequence). This fragment spans a 35 amino acid region defined by residues 22-46 of the TFIIB sequence.

Candidate inhibitor compounds from large libraries of synthetic or natural compounds can be screened. Numerous means are currently used for random and directed synthesis of saccharide, peptide, and nucleic acid based compounds. Synthetic compound libraries are commercially available from a number of companies including Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich (Milwaukee, WI). Combinatorial libraries are available and can

be prepared. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from e.g. Pan Laboratories (Bothell, WA) or MycoSearch (NC), or are readily produceable. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

Useful compounds may be found within numerous chemical classes, though typically they are organic compounds, and preferably small organic compounds. Small organic compounds have a molecular weight of more than 50 yet less than about 2,500 daltons, preferably less than about 750, more preferably less than about 350 daltons. Exemplary classes include heterocycles, peptides, saccharides, steroids, and the like. The compounds may be modified to enhance efficacy, stability, pharmaceutical compatibility, and the like. Structural identification of an agent may be used to identify, generate, or screen additional agents. For example, where peptide agents are identified, they may be modified in a variety of ways to enhance their stability, such as using an unnatural amino acid, such as a D-amino acid, particularly D-alanine, by functionalizing the amino or carboxylic terminus, e.g. for the amino group, acylation or alkylation, and for the carboxyl group, esterification or amidification, or the like. Other methods of stabilization may include encapsulation, for example, in liposomes, etc.

EXAMPLE 9

Measurement for effective inhibition

The amount of inhibition by a candidate inhibitor is quantified using the following formula, which describes reactions reconstituted with a radioactively labeled moiety:

$$\text{Percent Inhibition} = \frac{(CPM_{\text{Positive Control}} - CPM_{\text{Sample}})}{(CPM_{\text{Positive Control}})} \times 100$$

where $CPM_{\text{Positive Control}}$ is the average of the cpm in complexes or RNA molecules formed in reactions that lack the candidate inhibitor, and CPM_{Sample} is the cpm in complexes formed in reactions containing the candidate inhibitor. Candidate inhibitors for which the percent inhibition is 50% are titrated into reactions containing either _Candida albicans_

TFIIB or human TFIIB (expressed in and purified from *E. coli* using existing recombinant clones (Peterson et al., *Science* 248, 1625-1630, 1990; Kao et al., *Science* 248, 1646-1650, 1990; Hoffman, et al., *Nature* 346, 387-390, 1990, and assayed as described above) and their IC_{50} with respect to human and *Candida albicans* TFIIB determined from graphs of compound concentration vs. % inhibition. The IC_{50} is defined as the concentration that results in 50% inhibition. Candidate inhibitors for which the IC_{50} against *Candida albicans* TFIIB-containing reactions is less than or equal to 1/5 the IC_{50} against human TFIIB-containing reactions are further tested for their ability to inhibit the growth of *Candida albicans* in culture as described below.

EXAMPLE 10

Measurement for inhibition of *Candida albicans* growth in culture

Once an inhibitor is identified in one or more of the binding or transcription assays described herein, it may be desirable to determine the effect of the inhibitor on the growth and/or viability of *Candida albicans* in culture. A candidate inhibitor is tested for its ability to inhibit growth of *Candida albicans* cells in culture as follows. Methods for performing tests on growth inhibition in culture are well-known in the art. Once such procedure is based on the NCCLS M27P method (The National Committee for Clinical Laboratory Standards, Reference Method for Broth Dilution Antifungal Susceptibility Testing of Yeasts; proposed standard, 1992), as follows. Serial dilutions (two- or three-fold steps starting from a maximum concentration of 100 - 200 μg/ml) of candidate inhibitor are prepared using RPMI-1640 medium as diluent and an aliquot of 100 μl of each dilution is added to the wells of a 96-well polystyrene microtiter plate. Five *Candida albicans* colonies, picked from a Sabouraud Dextrose Agar plate inoculated 14-20 hr previously with the test *Candida albicans* strain (Catalog number 10231 from the American Type Culture Collection Yeast Catalog), are suspended with RAMI-1640 medium such that the density of cells is 10,000 - 30,000 cells/ml. 100u l of the cell suspension is added to each of the wells of the 96-well microtiter plate containing diluted candidate inhibitor and medium control. Cultures are mixed by agitation and incubated at 35°C for 48 hr without agitation, after which cell growth is monitored by visual inspection for the formation of turbidity and/or mycelial colonies. The minimum concentration of candidate inhibitor at which no cell growth is detected by this method is defined as the minimum inhibitory concentration (MIC) for that compound. Examples of MICs for

known antifungal compounds obtained using this technique are 0.125 - 0.5 µg/ml for fluconazole and 0.25 - 1.0 µg/ml for amphotericin B (The National Committee for Clinical Laboratory Standards, Reference Method for Broth Dilution Antifungal Susceptibility Testing of Yeasts; proposed standard, 1992). An inhibitor identified by the methods described herein, will have MIC which is equivalent to or less than the MICs for fluconazole or amphotericin B.

EXAMPLE 11

Transcription Inhibition Counterscreen Using Human TFIIB

A compound identified as an inhibitor of *Candida albicans* according to one or more of the assays described herein may be tested further in order to determine its effect on the host organism. In the development of useful antifungal compounds for human therapeutics, it is desirable that such compounds act as effective agents in inhibiting the viability of the fungal pathogen while not significantly inhibiting human cell systems. Specifically, inhibitors of *Candida albicans* identified in any one of the above described assays may be counterscreened for inhibition of human TFIIB.

Recombinant human TFIIB can be obtained from existing sources and purified by published methods (for example, see Peterson et al., Kao et al., and Hoffman et al., supra) and contacted with the candidate inhibitor in assays such as those described above using a human system. The effectiveness of a *Candida albicans* TFIIB inhibitor as a human therapeutic is determined as one which exhibits a low level of inhibition against human TFIIB relative to the level of inhibition with respect to *Candida albicans* TFIIB. For example, it is preferred that the amount of inhibition by a given inhibitor of human TFIIB in a human system be no more than 20% with respect to the amount of inhibition of *Candida albicans* TFIB in a *Candida* system when tested in any of the assays described above.

Dosage and Pharmaceutical Formulations

For therapeutic uses, inhibitors identified as described herein may be administered in a pharmaceutically acceptable/biologically compatible formulation, for example, in the form of a cream, ointment, lotion or spray for topical use, or in a physiological solution, such as a salt solution, for internal administration. The amount of inhibitor administered will be determined according to the degree of pathogenic

infection and whether the infection is systemic or localized, and will typically be in the range of about 1ug - 100 mg/kg body weight. Where the inhibitor is a peptide or polypeptide, it will be administered in the range of about 100 - 500 ug/ml per dose. A single dose of inhibitor or multiple doses, daily, weekly, or intermittently, is contemplated according to the invention.

The route of administration will be chosen by the physician, and may be topical, oral, transdermal, nasal, rectal, intravenous, intramuscular, or subcutaneous.

Budapest Treaty Deposit

E. coli transformed with a plasmid containing the gene encoding *Candida albicans* TBP has been deposited in an international depository, the A.T.C.C., Rockville, MD, under the accession number 69900, on September 15, 1995. *E. coli* transformed with a plasmid containing the gene encoding *Candida albicans* TFIIB has been deposited in an international depository, the A.T.C.C., Rockville, MD, under the accession number 69899, on September 15, 1995. A.T.C.C. Nos. 69900 and 69889 will be available to the public upon the grant of a patent which discloses the accession numbers in conjunction with the invention described herein. The deposits were made under the Budapest Treaty, will be available beyond the enforceable life of the patent for which the deposit is made, and will be maintained for a period of at least 30 years from the time of deposit and at least 5 years after the most recent request for the furnishing of a sample of the deposit is received by the A.T.C.C. It is to be understood that the availability of these deposits does not constitute a license to practice the subject invention in derogation of patent rights granted for the subject invention by governmental action.

OTHER EMBODIMENTS

The foregoing examples demonstrate experiments performed and contemplated by the present inventors in making and carrying out the invention. It is believed that these examples include a disclosure of techniques which serve to both apprise the art of the practice of the invention and to demonstrate its usefulness. It will be appreciated by those of skill in the art that the techniques and embodiments disclosed herein are preferred embodiments only that in general numerous equivalent methods and techniques may be employed to achieve the same result.

All of the references identified hereinabove, are hereby expressly incorporated herein by reference to the extent that they describe, set forth, provide a basis for or enable compositions and/or methods which may be important to the practice of one or more embodiments of the present inventions.

5

5   SEQUENCE LISTING

                 (1) GENERAL INFORMATION

10   (i) APPLICANT: SCRIPTGEN PHARMACEUTICALS, INC.

                 (ii) TITLE OF THE INVENTION: NOVEL TFIIB TRANSCRIPTION FACTOR FROM
         CANDIDA ALBICANS...

15   (iii) NUMBER OF SEQUENCES: 4

                 (iv) CORRESPONDENCE ADDRESS:
                    (A) ADDRESSEE: DARBY & DARBY P.C.
                    (B) STREET: 805 Third Avenue
20   (C) CITY: New York
                    (D) STATE: New York
                    (E) COUNTRY: United States of America
                    (F) ZIP: 10022-7513

25   (v) COMPUTER READABLE FORM:
                    (A) MEDIUM TYPE: Diskette
                    (B) COMPUTER: IBM Compatible
                    (C) OPERATING SYSTEM: DOS
                    (D) SOFTWARE: FastSEQ Version 1.5
30
                 (vi) CURRENT APPLICATION DATA:
                    (A) APPLICATION NUMBER:
                    (B) FILING DATE:
                    (C) CLASSIFICATION:
35
                 (vii) PRIOR APPLICATION DATA:
                    (A) APPLICATION NUMBER: 08/625,377
                    (B) FILING DATE: 01-APR-1996

40

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                    (B) REGISTRATION NUMBER: 25,351
45   (C) REFERENCE/DOCKET NUMBER: 0342/2C488-WO

                 (ix) TELECOMMUNICATION INFORMATION:
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                    (B) TELEFAX: (212)753-6237
50   (C) TELEX:

                 (2) INFORMATION FOR SEQ ID NO:1:

55   (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 219 amino acids
                    (B) TYPE: amino acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear
60
                 (ii) MOLECULE TYPE: peptide
                 (iii) HYPOTHETICAL: NO
                 (iv) ANTISENSE: NO
                 (v) FRAGMENT TYPE: internal
65   (vi) ORIGINAL SOURCE:

                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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         50                  55                  60
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     65                  70                  75                  80
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                     85                  90                  95
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(2) INFORMATION FOR SEQ ID NO:2:

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        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE: internal
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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  5     Lys Thr Asn Val Pro Arg Lys Glu Ile Gly Lys Val Phe Lys Ile Met
                    195                     200                 205
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             210                     215                 220
        Tyr Gly Gln Asp Ser Ile Gln Thr Thr Gln Thr Ser Ala Glu Asp Leu
 10     225                     230                     235             240
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                        245                     250                 255
        Gly Ala Glu Tyr Ile Ala Arg Arg Cys Lys Glu Val Gly Val Leu Ala
                    260                     265                 270
 15     Gly Arg Ser Pro Thr Thr Ile Ala Ala Thr Val Ile Tyr Met Ala Ser
                    275                     280                 285
        Leu Val Phe Gly Phe Asp Leu Pro Pro Ser Lys Ile Ser Asp Lys Thr
             290                     295                 300
        Gly Val Ser Asp Gly Thr Ile Lys Thr Ser Tyr Lys Tyr Met Tyr Glu
 20     305                     310                     315             320
        Glu Lys Glu Gln Leu Ile Asp Pro Ser Trp Ile Glu Ser Gly Lys Val
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        Lys Leu Glu Lys Ile Pro Lys Asn
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 25
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            (2) INFORMATION FOR SEQ ID NO:3:

            (i) SEQUENCE CHARACTERISTICS:
 30   (A) LENGTH: 657 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

 35   (ii) MOLECULE TYPE: cDNA
            (iii) HYPOTHETICAL: NO
            (iv) ANTISENSE: NO
            (v) FRAGMENT TYPE:
            (vi) ORIGINAL SOURCE:
 40
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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 45     GGTATAGTGC CCACATTACA AAATATTCTT GCTACGGTGA ATCTTGATTG TCGACTTGAT   180
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        ATTCAAAAGT TGGGGTTCAA TGCTAAATTT TGTGATTTTA AAATTCAAAA TATAGTGGGG   420
 50     TCAACAGATG TTAAGTTTGC TATTAGATTA GAAGGCTTAG CTTTTGCTCA TGGTACTTTT   480
        TCTTCATATG AACCAGAATT ATTTCCTGGG TTAATTTATA GAATGGTGAA ACCAAAAATT   540
        GTTTTACTTA TATTTGTTTC TGGGAAAATT GTTTTGACGG GTGCCAAAAA GACAGAAGAA   600
        ATTTATGATG CATTTGAACT GATTTATCCG GTTTTAAATG AATTTCGTAA AAATTGA      657
```

 55
            (2) INFORMATION FOR SEQ ID NO:4:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1095 base pairs
 60   (B) TYPE: nucleic acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY:

```
        (ii)  MOLECULE TYPE:
        (iii) HYPOTHETICAL: NO
        (iv)  ANTISENSE: NO
        (v)   FRAGMENT TYPE:
  5     (vi)  ORIGINAL SOURCE:

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:4:

      TAAGCTTGTA TTACTAAGCA TATTATGTCG CCATCAACAT CTACGGCAGT ACAGGAGTAT      60
 10   ATTGGACCAA ACTTGAATGT TACATTAACA TGTCCTGAGT GTAAGATATT TCCACCTGAT     120
      TTGGTAGAGA GGTTCAGCGA AGGTGACATT GTCTGTGGCA GTTGTGGGCT AGTATTGAGT     180
      GATCGTGTTG TGGATACGAG ATCAGAATGG AGAACTTTCA GTAACGATGA CCAAAATGGT     240
      GATGATCCTT CTCGTGTTGG TGATGCAGGT AACCCTTTAT TAGACACAGA GGACTTGTCC     300
      ACAATGATTT CTTATGCTCC TGATACTACC AAAGCAGGAA GAGAGTTAAG CCGAGCCCAA     360
 15   TCTAAATCTC TAGTCGATAA AAAAGACAAT GCATTGGCTG CAGCATATAT CAAGATTTCT     420
      CAAATGTGCG ATGGTTATCA ATTGCCTAAA ATAGTTCTGG ATGGGGCCAA GGAAGTCTAC     480
      AAAATGGTTT ATGACGAGAA ACCATTGCGA GGAAAATCAC AAGAGAGTAT CATGGCAGCT     540
      TCTATCTTTA TTGGTTGCAG AAAGGCCAAT GTTGCTCGTT CATTCAAAGA GATATGGGCA     600
      AAGACTAATG TACCTCGTAA GGAAATTGGT AAAGTGTTCA AGATCATGGA CAAGATCATT     660
 20   CGTGAAAAGA ATGCAGCCAA CCCTAATGCT GCATATTACG GTCAAGACAG CATTCAAACC     720
      ACCCAAACTT CGGCCGAGGA TTTGATTAGA AGATTCTGTT CTCACTTGGG TGTTAACACA     780
      CAAGTTACAA ATGGTGCGGA ATACATAGCC AGAAGATGTA AGGAAGTCGG GGTTTTAGCA     840
      GGTAGATCGC CAACTACAAT TGCTGCAACT GTAATTTACA TGGCTTCACT AGTGTTTGGA     900
      TTTGACTTAC CTCCATCCAA GATATCTGAT AAAACTGGTG TCAGTGATGG TACTATCAAA     960
 25   ACTTCATACA AGTACATGTA CGAGGAGAAA GAACAATTGA TTGATCCATC TTGGATAGAA    1020
      AGTGGTAAAG TAAAATTGGA AAAAATACCA AAAAACTAAT ACAGCGGAGT CGCCACTGTT    1080
      AATCCTTTAC CCTCT                                                     1095
```

CLAIMS

1.   A recombinant nucleic acid comprising a nucleic acid sequence encoding *Candida albicans* TFIIB.

2.   A vector comprising a nucleic acid sequence encoding *Candida albicans* TFIIB.

3.   A transformed host cell containing a nucleic acid sequence encoding *Candida albicans* TFIIB.

4.   A recombinant polypeptide comprising *Candida albicans* TFIIB.

5.   A fragment of *Candida albicans* TFIIB, said fragment being characterized in that it inhibits the biological activity of *Candida albicans* TFIIB in transcription initiation.

6.   A fragment of *Candida albicans* TFIIB, said fragment being characterized in that it prevents the growth of *Candida albicans* .

7.   A method for producing recombinant *Candida albicans* TFIIB, comprising culturing the host cell of claim 3 under conditions sufficient to permit expression of the nucleic acid encoding *Candida albicans* TFIIB, and isolating said *Candida albicans* TFIIB.

8.   A screening method for identifying an inhibitor of *Candida albicans* growth, comprising detecting inhibition of mRNA transcription in an *in vitro* transcription assay comprising a DNA template, RNA polymerase II, recombinant *Candida albicans* TFIIB, and a candidate inhibitor, wherein production of an mRNA transcript from said DNA template occurs in the absence if said candidate inhibitor.

9.   A screening method for identifying an inhibitor of _Candida albicans_ growth, comprising detecting in the presence of a candidate inhibitor inhibition of formation of a complex comprising a DNA template and recombinant _Candida albicans_ TFIIB, wherein in the absence of said candidate inhibitor, formation of said complex occurs.

10.   A screening method for identifying an inhibitor of _Candida albicans_ growth, comprising detecting in the presence of a candidate inhibitor inhibition of formation of a complex comprising _Candida albicans_ TFIIB and _Candida albicans_ TBP, wherein in the absence of said candidate inhibitor formation of said complex occurs.

11.   A screening method for identifying an inhibitor of _Candida albicans_ growth, comprising detecting in the presence of a candidate inhibitor inhibition of formation of a complex comprising RNA polymerase II, _Candida albicans_ TBP, and _Candida albicans_ TFIIB, wherein in the absence of said candidate inhibitor formation of said complex occurs.

12.   The screening method of claim 8, 9, 10 or 11, wherein said detecting is performed in the presence of a plurality of candidate inhibitors such that said inhibition is indicative of inhibition by a said candidate inhibitor of said plurality.

13.   The screening method of claim 8, 9, 10, or 11, wherein multiple detecting steps are performed simultaneously using a plurality of candidate inhibitors, wherein detection of inhibition by any one candidate inhibitor is detectable independently of said plurality.

14.   A method of preventing _Candida albicans_ growth in culture, comprising contacting said culture with an inhibitor that selectively inhibits the biological activity of _Candida albicans_ TFIIB.

15.   A method of preventing _Candida albicans_ growth in a mammal, comprising contacting said mammal with an inhibitor that selectively inhibits the biological activity of _Candida albicans_ TFIIB.

FIG. IA

```
  1 ATG GAT TTA AAA CCC CCA ACT AAT CCA CAA GCA AAG ACT TTT ATG                 60
  1  M   D   L   K   P   P   T   N   P   Q   A   K   T   F   M                    20

 61 AAG TCA ATA GAG GAA GAT GAA AAA AAT GCC GAA GAT ATT ATA AAA AAG GAA         120
 21  K   S   I   E   E   D   E   K   N   A   E   D   I   I   K   K   E            40

121 GAC ATT GAT GAA CCT AAA CAA GAA GAT CAA GAT ACC ACT GAT AGT AAT GGT GGA GGT 180
 41  D   I   D   E   P   K   Q   E   D   Q   D   T   T   D   S   N   G   G   G    60

181 ATA GTG CCC ACA TTA CAA AAT ATT GTT GCT ACG GTG AAT CTT GAT TGT CGA CTT GAT 240
 61  I   V   P   T   L   Q   N   I   V   A   T   V   N   L   D   C   R   L   D    80

241 AAA ACA ATT GCT TTA CAT GCT AGA AAT GCC GAA TAT AAT CCA AAA CGT TTT GCT GCG GTG 300
 81  K   T   I   A   L   H   A   R   N   A   E   Y   N   P   K   R   F   A   V    100

301 ATT ATG AGA ATT AGA GAT CCA AAA ACT ACG GCA TTA ATC TTT GCT TCG GGG AAA ATG GTT 360
101  I   M   R   I   R   D   P   K   T   T   A   L   I   F   A   S   G   K   M   V 120
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A—————————————————————————————A

FIG. 1B

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A ──────────────────────────────────────────────────────────────────────────  A

361 GTG ACT GGG GCT AAA TCC GAA GAT GAT TCC AAG TTG GCT TCA AGA AAG TAT GCT AGA ATC 420
121  V   T   G   A   K   S   E   D   D   S   K   L   A   S   R   K   Y   A   R   I  140

421 ATT CAA AAG TTG GGG TTC AAT GCT AAA TTT TGT GAT TTT AAA ATT CAA AAT ATA GTG GGG 480
141  I   Q   K   L   G   F   N   A   K   F   C   D   F   K   I   Q   N   I   V   G  160

481 TCA ACA GAT GTT AAG TTT GCT ATT AGA TTA GAA GGC TTA GCT TTT GCT CAT GGT ACT TTC 540
161  S   T   D   V   K   F   A   I   R   L   E   G   L   A   F   A   H   G   T   F  180

541 TCT TCA TAT GAA CCA TTA TTT CCT GGG TTA ATT TAT AGA ATG GTG AAA CCA AAA ATT 600
181  S   S   Y   E   P   L   F   P   G   L   I   Y   R   M   V   K   P   K   I   200

601 GTT TTA CTT ATA TTT GTT TCT GGG AAA ATT GTT TTG ACG GGT GCC AAA AAG AGA GAA GAA 660
201  V   L   L   I   F   V   S   G   K   I   V   L   T   G   A   K   K   R   E   E  220

661 ATT TAT GAT GCA TTT GAA CTG ATT TAT CCG GTT TTA AAT GAA TTT CGT AAA AAT TGA 717
221  I   Y   D   A   F   E   S   I   Y   P   V   L   N   E   F   R   K   N   *  239
```

FIG. 2A

```
1   TAAGCTTGTATTACTAAGGATATT ATG TCG CCA TCA ACA TCT ACG GCA GTA CAG GAG TAT ATT GGA  66
1                            M   S   P   S   T   S   T   A   V   Q   E   Y   I   G    14

67  CCA AAC TTG AAT GTT ACA TTA ACA TGT CCT GAG TGT AAG ATA TTT CCA CCT GAT TTG GTA  126
15  P   N   L   N   V   T   L   T   C   P   E   C   K   I   F   P   P   D   L   V    34

127 GAG AGG TTC AGC GAA GGT GAC ATT GTC TGT GGC AGT TGT GGG CTA GTA TTG AGT GAT CGT  186
35  E   R   F   S   E   G   D   I   V   C   G   S   C   G   L   V   L   S   D   R    54

187 GTT GTG GAT ACG AGA TCA GAA TGG AGA ACT TTC AGT AAC GAT GAC CAA AAT GGT GAT GAT  246
55  V   V   D   T   R   S   E   W   R   T   F   S   N   D   D   Q   N   G   D   D    74

247 CCT TCT CGT GTT GGT GAT GCA GGT AAC CCT TTA TTA GAC ACA GAG GAC TTG TCC ACA ATG  306
75  P   S   R   V   G   D   A   G   N   P   L   L   D   T   E   D   L   S   T   M    94

307 ATT TCT TAT GCT CCT GAT AGT ACC AAA GCA GGA AGA GAG TTA AGC CGA GCC CAA TCT AAA  366
95  I   S   Y   A   P   D   S   T   K   A   G   R   E   L   S   R   A   Q   S   K    114

367 TCT CTA GTC GAT AAA AAA GAC AAT GCA TTG GCT GCA TAT ATC AAG ATT TCT CAA ATG      426
115 S   L   V   D   K   K   D   N   A   L   A   A   Y   I   K   I   S   Q   M        134

427 TGC GAT GGT TAT CAA TTG CCT AAA ATA GTT CTG GAT GGG GCC AAG GAA GTC TAC AAA ATG  486
135 C   D   G   Y   Q   L   P   K   I   V   S   D   G   A   K   E   V   Y   K   M    154

487 GTT TAT GAC GAG AAA CCA TTG CGA GGA AAA TCA CAA GAG AGT ATC ATG GCA GCT TCT ATC  546
155 V   Y   D   E   K   P   L   R   G   K   S   Q   E   S   I   M   A   A   S   I    174
```

FIG. 2B

```
547  TTT ATT GGT TGC AGA AAG GCC AAT GTT GCT CGT TCA TTC AAA GAG ATA TGG GCA AAG ACT  606
175   F   I   G   C   R   K   A   N   V   A   R   S   F   K   E   I   W   A   K   T   194

607  AAT GTA CCT CGT AAG GAA ATT GGT AAA GTG TTC AAG ATC ATG GAC AAG ATC ATT CGT GAA  666
195   N   V   P   R   K   E   I   G   K   V   F   K   I   M   D   K   I   I   R   E   214

667  AAG AAT GCA GCC AAC CCT AAT GCT CAA TAT TAC GGT CAA GAC AGC ATT CAA ACC ACC CAA  726
215   K   N   A   A   N   P   N   A   Q   Y   Y   G   Q   D   S   I   Q   T   T   Q   234

727  ACT TCG GCC GAG GAT TTG ATT AGA AGA TTC TGT TCT CAC TTG GGT GTT AAC ACA CAA GTT  786
235   T   S   A   E   D   L   I   R   R   F   C   S   H   L   G   V   N   T   Q   V   254

787  ACA AAT GGT GCG GAA TAC ATA GCC AGA AGA TGT AAG GAA GTC GGG GTT TTA GCA GGT AGA  846
255   T   N   G   A   E   Y   I   A   R   R   C   K   E   V   G   V   L   A   G   R   274

847  TCG CCA ACT ACA ATT GCT GCA ACT GTA ATT TAC ATG GCT GTC CTA GTG TTT GGA TTT GAC  906
275   S   P   T   T   I   A   A   T   V   I   Y   M   A   S   L   V   F   G   F   D   294

907  TTA CCT CCA TCC AAG ATA TCT GAT AAA ACT GGT GTC AGT GAT GGT ATC AAA ACT TCA      966
295   L   P   P   S   K   I   S   D   K   T   G   V   S   D   G   T   I   K   T   S   314

967  TAC AAG TAC ATG TAC GAG GAG AAA GAA CAA TTG ATT GAT CCA TCT TGG ATA GAA AGT GGT 1026
315   Y   K   Y   M   Y   E   E   K   E   Q   L   I   D   P   S   W   I   E   S   G   334

1027 AAA GTA AAA TTG GAA AAA ATA CCA AAA AAC TAA TACAGCGGAGTGCCACTGTTAATCCTTTACCCTCT 1095
335   K   V   K   L   E   K   I   P   K   N   *                                        345
```

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.
US CL   :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 23.74; 435/320.1, 252.3, 325, 172.3, 69.1, 6, 7.1; 530/350, 300; 514/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG - Biotech Files

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KHOO et al. Conserved functional domains of the RNA polymerase III general trasncription factor BRF. Genes and Development. 1994, Vol. 8, pages 2879-2890, see entire document.	1-15
Y	NA et al. The Kluyveromyces gene encoding the general transcription factor IIB: structural analysis and expression in Saccharomyces cerevisiae. Nucleic Acids Research. 1993, Vol. 21, No. 15, pages 3413-3417, see entire document.	1-15

[X] Further documents are listed in the continuation of Box C.   [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"E"	earlier document published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
04 AUGUST 1997	2 9 AUG 1997
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer ELIZABETH C. KEMMERER
Facsimile No. (703) 305-3230	Telephone No. (703) 308-6196

Form PCT/ISA/210 (second sheet)(July 1992)*

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	PINTO et al. Characterization of sua7 mutations defines a domain of TFIIB involved in transcription start site selection in yeast. Journal of Biological Chemistry. 1994, Vol. 269, No. 48, pages 30569-30573, see entire document.	1-15
Y	LOPEZ-DE-LEON et al. PCF4 encodes an RNA polymerase III trsancription factor with homology to TFIIB. Cell. 16 October 1992, Vol. 71, pages 211-220, see entire document.	1-15
Y	KILLEEN et al. Recombinant TBP, transcription factor IIB, and RAP30 are sufficient for promoter recognition by mammalian RNA polymerase II. Journal of Biological Chemistry. 15 May 1992, Vol. 267, No. 14, pages 9463-9466, see entire document.	1-15
Y	PINTO et al. The yeast sua7 gene encodes a homolog of human transcription factor TFIIB and is required for normal start site delection in vivo. Cell. 06 March 1992, Vol. 68, pages 977-988, see entire document.	1-15
Y	MONCOLLIN et al. Class II (B) general transcription factor (TFIIB) that binds to the template-committed preinitiation complex is different from general transcription factor BTF3. Proceedings of the National Academy of Sciences USA. January 1992, Vol. 89, pages 397-401, see entire document.	1-15
Y	COLBERT et al. A yeast TFIIB-related factor involved in RNA polymerase III transcription. Genes and Development. 1992, Vol. 6, pages 1940-1949, see entire document.	1-15
A	HAHN et al. Isolation of the gene encoding the yeast TATA binding protein TFIID: a gene identical o the SPT15 suppressor of Ty element insertions. Cell. 22 September 1989, Vol. 58, pages 1173-1181, see entire document.	1-15
Y	HORIKOSHI et al. Cloning and structure of a yeast gene encoding a general transcription initiation factor TFIID that binds to the TATA box. Nature. 28 September 1989, Vol. 341, pages 299-303, see entire document.	1-15
A	FIKES et al. Striking conservation of TFIID in Schizosaccharomyces pombe and Saccharomyces cerevisiae. Nature. 19 July 1990, Vol. 346, pages 291-294, see entire document.	1-15
A	SCHMIDT et al. Yeast TATA-box transcription factor gene. Proceedings of the National Academy of Sciences USA. October 1989, Vol. 86, pages 7785-7789, see entire document.	1-15

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

G01N 33/68, 37/00; A61K 38/16; C07K 14/40; C12N 5/10, 15/31, 15/63

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

536/23.1, 23.74; 435/320.1, 252.3, 325, 172.3, 69.1, 6, 7.1; 530/350, 300; 514/2